

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/807, 517
Source: 1Fw9
Date Processed by STIC: 4/11/06

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/807,517

DATE: 04/11/2006

TIME: 11:09:28

Input Set : D:\P-2762-US3.txt

Output Set: N:\CRF4\04112006\J807517.raw

3 <110> APPLICANT: GTx, Inc.
 4 et al.,, Steiner
 5 Steiner, Et al.,
 7 <120> TITLE OF INVENTION: ISOLATED NUCLEIC ACIDS ENCODING RAT P-HYDE PROTEIN
 9 <130> FILE REFERENCE: P-2762-US3
 C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/807,517
 C--> 11 <141> CURRENT FILING DATE: 2004-03-24
 11 <160> NUMBER OF SEQ ID NOS: 9
 13 <170> SOFTWARE: PatentIn version 3.3
 15 <210> SEQ ID NO: 1
 16 <211> LENGTH: 1886
 17 <212> TYPE: DNA
 18 <213> ORGANISM: Human
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25	cccgatgagg	cccccaaagt	gagcatcctg	ggtagcgggg	actttgcccg	ctccctggcc	180
27	acacgcctgg	tgggctctgg	cttcaaagtg	gtggtgggga	gccgcaaccc	caaacgcaca	240
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31	gaggtcatct	ttgtggctgt	gttccgggag	cactactctt	cactgtgcag	tctcagtgac	360
33	cagctggcgg	gcaagatcct	ggtggatgtg	agcaacccta	cagagcaaga	gcaccttcag	420
35	catcgtgagt	ccaatgctga	gtacctggcc	tccctcttcc	ccacttgcac	agtgggtcaag	480
37	gccttcaatg	tcattctctg	ctggaccctg	caggctggcc	caagggatgg	taacgggcag	540
39	gtgcccattc	gcggtgacca	gccagaagcc	aagcgtgctg	tctcggagat	ggcgctcgcc	600
41	atgggcttca	tgcccgtgga	catgggatcc	ctggcgctcag	cctgggaggt	ggaggccatg	660
43	cccctgcgcc	tcctcccggc	ctggaagggt	cccaccctgc	tggccctggg	gctcttcgtc	720
45	tgcttctatg	cctacaactt	cgtccgggac	gttctgcagc	cctatgtgca	ggaaagccag	780
47	aacaagttct	tcaagctgcc	cgtgtccgtg	gtcaacacca	cactgccgtg	cgtggcctac	840
49	gtgctgctgt	cactcgtgta	cttgcccggc	gtgctggcgg	ctgccctgca	gctgcggcgc	900
51	ggcaccaagt	accagcgtt	ccccgactgg	ctggaccact	ggctacagca	ccgcaagcag	960
53	atcgggctgc	tcagcttctt	ctgcgcgcgc	ctgcacgccc	tctacagctt	ctgcttgccg	1020
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65	ttctacctgc	ctcccacctt	cacgctcacg	ctgctgggtg	cctgcgtcgt	catcctggcc	1380
67	aaagccctgt	ttctcctgcc	ctgcatcagc	cgcagactcg	ccaggatccg	gagaggctgg	1440
69	gagagggaga	gcaccatcaa	gttcacgctg	cccacagacc	acgccctggc	cgagaagacg	1500
71	agccacgtat	gaggtgcctg	ccctgggctc	tggaccccg	gcacacgagg	gacgggtgcc	1560
73	tgagcccgtt	aggttttctt	ttcttggtgg	tgcaaagtgg	tataactgtg	tgcaaataag	1620
75	aggttttgagg	tccaaattcc	tgggactcaa	atgtatgcag	tactattcag	aatgatatac	1680
77	acacatatgt	gtatatgtat	ttacatatat	tccacatata	taacaggatt	tgcaattata	1740

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101 Ile Leu Gly Ser Gly Asp Phe Ala Arg Ser Leu Ala Thr Arg Leu Val
102 35 40 45
105 Gly Ser Gly Phe Lys Val Val Val Gly Ser Arg Asn Pro Lys Arg Thr
106 50 55 60
109 Ala Arg Leu Phe Pro Ser Ala Ala Gln Val Thr Phe Gln Glu Glu Ala
110 65 70 75 80
113 Val Ser Ser Pro Glu Val Ile Phe Val Ala Val Phe Arg Glu His Tyr
114 85 90 95
117 Ser Ser Leu Cys Ser Leu Ser Asp Gln Leu Ala Gly Lys Ile Leu Val
118 100 105 110
121 Asp Val Ser Asn Pro Thr Glu Gln Glu His Leu Gln His Arg Glu Ser
122 115 120 125
125 Asn Ala Glu Tyr Leu Ala Ser Leu Phe Pro Thr Cys Thr Val Val Lys
126 130 135 140
129 Ala Phe Asn Val Ile Ser Ala Trp Thr Leu Gln Ala Gly Pro Arg Asp
130 145 150 155 160
133 Gly Asn Gly Gln Val Pro Ile Cys Gly Asp Gln Pro Glu Ala Lys Arg
134 165 170 175
137 Ala Val Ser Glu Met Ala Leu Ala Met Gly Phe Met Pro Val Asp Met
138 180 185 190
141 Gly Ser Leu Ala Ser Ala Trp Glu Val Glu Ala Met Pro Leu Arg Leu
142 195 200 205
145 Leu Pro Ala Trp Lys Val Pro Thr Leu Leu Ala Leu Gly Leu Phe Val
146 210 215 220
149 Cys Phe Tyr Ala Tyr Asn Phe Val Arg Asp Val Leu Gln Pro Tyr Val
150 225 230 235 240
153 Gln Glu Ser Gln Asn Lys Phe Phe Lys Leu Pro Val Ser Val Val Asn
154 245 250 255
157 Thr Thr Leu Pro Cys Val Ala Tyr Val Leu Leu Ser Leu Val Tyr Leu
158 260 265 270
161 Pro Gly Val Leu Ala Ala Ala Leu Gln Leu Arg Arg Gly Thr Lys Tyr
162 275 280 285
165 Gln Arg Phe Pro Asp Trp Leu Asp His Trp Leu Gln His Arg Lys Gln
166 290 295 300
169 Ile Gly Leu Leu Ser Phe Phe Cys Ala Ala Leu His Ala Leu Tyr Ser
170 305 310 315 320
173 Phe Cys Leu Pro Leu Arg Arg Ala His Arg Tyr Asp Leu Val Asn Leu

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174		325		330		335
177	Ala Val Lys Gln Val Leu Ala Asn Lys Ser His Leu Trp Val Glu Glu					
178		340		345		350
181	Val Trp Arg Met Glu Ile Tyr Leu Ser Leu Gly Val Leu Ala Leu Gly					
182		355		360		365
185	Thr Leu Ser Leu Leu Ala Val Thr Ser Leu Pro Ser Ile Ala Asn Ser					
186		370		375		380
189	Leu Asn Trp Arg Glu Phe Ser Phe Val Gln Ser Ser Leu Gly Phe Val					
190	385		390		395	400
193	Ala Leu Val Leu Ser Thr Leu His Thr Leu Thr Tyr Gly Trp Thr Arg					
194		405		410		415
197	Ala Phe Glu Glu Ser Arg Tyr Lys Phe Tyr Leu Pro Pro Thr Phe Thr					
198		420		425		430
201	Leu Thr Leu Leu Val Pro Cys Val Val Ile Leu Ala Lys Ala Leu Phe					
202		435		440		445
205	Leu Leu Pro Cys Ile Ser Arg Arg Leu Ala Arg Ile Arg Arg Gly Trp					
206		450		455		460
209	Glu Arg Glu Ser Thr Ile Lys Phe Thr Leu Pro Thr Asp His Ala Leu					
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214 485

217 <210> SEQ ID NO: 3

218 <211> LENGTH: 2118

219 <212> TYPE: DNA

220 <213> ORGANISM: Human

222 <400> SEQUENCE: 3

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227	cccgatgagg	cccccaaagt	gagcatcctg	ggtagcgggg	actttgcccg	ctccctggcc	180
229	acacgcctgg	tgggctctgg	cttcaaagtg	gtggtgggga	gccgcaacc	caaacgcaca	240
231	gccaggctgt	ttccctcagc	ggcccaaagt	actttccaag	aggaggcagt	gagctccccg	300
233	gaggtcatct	ttgtggctgt	gttccgggag	cactactctt	cactgtgcag	tctcagtgc	360
235	cagctggcgg	gcaagatcct	ggtggatgtg	agcaacccta	cagagcaaga	gcaccttcag	420
237	catcgtgagt	ccaatgctga	gtacctggcc	tccctcttcc	ccacttgcac	agtggccaag	480
239	gccttcaatg	tcatctctgc	ctggaccctg	caggctggcc	caagggatgg	taacggggcag	540
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259	aagagccacc	tctgggtgga	ggaggtctgg	cggatggaga	tctacctctc	cctgggagtg	1140
261	ctggccctcg	gcacgttgtc	cctgctggcc	gtgacctcac	tgccgtccat	tgcaaactcg	1200
263	ctcaactgga	gggagttcag	cttcgttcag	tgtgtggcaa	cttccagtgc	aggaaacaca	1260
265	ggcagtggaa	cccgaagacc	tgaatctcag	tccaagacc	cccacttacc	tgccccgcat	1320
267	catcagacaa	gtttcctagg	ccctcggagc	ttctgctgct	cacttgtgcc	tgtgtccacc	1380

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273 gcacacgctc acctacggct ggacccgcgc cttcgaggag agccgctaca agttctacct 1560
275 gcctcccacc ttcacgctca cgctgctggt gccctgcgtc gtcattcctgg ccaaagccct 1620
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279 gagcaccatc aagttcacgc tgcccacaga ccacgccctg gccgagaaga cgagccacgt 1740
281 atgaggtgcc tgccctgggc tctggacccc gggcacacga gggacggtgc cctgagcccg 1800
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285 ggtccaaatt cctgggactc aaatgtatgc agtactattc agaatgatat acacacatat 1920
287 gtgtatatgt atttacatat attccacata tataacagga tttgcaatta tacatagcta 1980
289 gctaaaaagt tgggtctctg agatttcaac ttgtagattt aaaaacaagt gccgtacgtt 2040
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311 Ile Leu Gly Ser Gly Asp Phe Ala Arg Ser Leu Ala Thr Arg Leu Val
312 35 40 45
315 Gly Ser Gly Phe Lys Val Val Val Gly Ser Arg Asn Pro Lys Arg Thr
316 50 55 60
319 Ala Arg Leu Phe Pro Ser Ala Ala Gln Val Thr Phe Gln Glu Glu Ala
320 65 70 75 80
323 Val Ser Ser Pro Glu Val Ile Phe Val Ala Val Phe Arg Glu His Tyr
324 85 90 95
327 Ser Ser Leu Cys Ser Leu Ser Asp Gln Leu Ala Gly Lys Ile Leu Val
328 100 105 110
331 Asp Val Ser Asn Pro Thr Glu Gln Glu His Leu Gln His Arg Glu Ser
332 115 120 125
335 Asn Ala Glu Tyr Leu Ala Ser Leu Phe Pro Thr Cys Thr Val Val Lys
336 130 135 140
339 Ala Phe Asn Val Ile Ser Ala Trp Thr Leu Gln Ala Gly Pro Arg Asp
340 145 150 155 160
343 Gly Asn Gly Gln Val Pro Ile Cys Gly Asp Gln Pro Glu Ala Lys Arg
344 165 170 175
347 Ala Val Ser Glu Met Ala Leu Ala Met Gly Phe Met Pro Val Asp Met
348 180 185 190
351 Gly Ser Leu Ala Ser Ala Trp Glu Val Glu Ala Met Pro Leu Arg Leu
352 195 200 205
355 Leu Pro Ala Trp Lys Val Pro Thr Leu Leu Ala Leu Gly Leu Phe Val
356 210 215 220
359 Cys Phe Tyr Ala Tyr Asn Phe Val Arg Asp Val Leu Gln Pro Tyr Val
360 225 230 235 240
363 Gln Glu Ser Gln Asn Lys Phe Phe Lys Leu Pro Val Ser Val Val Asn

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364		245		250		255
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372		275		280		285
375	Gln Arg Phe Pro Asp Trp Leu Asp His Trp Leu Gln His Arg Lys Gln					
376		290		295		300
379	Ile Gly Leu Leu Ser Phe Phe Cys Ala Ala Leu His Ala Leu Tyr Ser					
380	305		310		315	320
383	Phe Cys Leu Pro Leu Arg Arg Ala His Arg Tyr Asp Leu Val Asn Leu					
384		325		330		335
387	Ala Val Lys Gln Val Leu Ala Asn Lys Ser His Leu Trp Val Glu Glu					
388		340		345		350
391	Val Trp Arg Met Glu Ile Tyr Leu Ser Leu Gly Val Leu Ala Leu Gly					
392		355		360		365
395	Thr Leu Ser Leu Leu Ala Val Thr Ser Leu Pro Ser Ile Ala Asn Ser					
396		370		375		380
399	Leu Asn Trp Arg Glu Phe Ser Phe Val Gln Cys Val Ala Thr Ser Ser					
400	385		390		395	400
403	Ala Gly Asn Thr Gly Ser Gly Thr Arg Arg Pro Glu Ser Gln Ser Gln					
404		405		410		415
407	Asp Pro His Leu Pro Ala Pro His His Gln Thr Ser Phe Leu Gly Pro					
408		420		425		430
411	Arg Ser Phe Cys Cys Ser Leu Val Pro Val Ser Thr Pro Tyr Gly His					
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415	Gln Glu Asp Leu Ser Trp Thr Arg					
416		450		455		

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420 <211> LENGTH: 2714

421 <212> TYPE: DNA

422 <213> ORGANISM: Rat

424 <400> SEQUENCE: 5

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429	agtgggcatc ctgggcagcg gggattttgc ccggtccctg gccacacgcc tgggtgggctc	180
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VERIFICATION SUMMARY

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L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date